

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.

(ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

(iii) NUMBER OF SEQUENCES: 11

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 460 Point San Bruno Blvd

(C) CITY: South San Francisco

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(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

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(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 31-Mar-1997

(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1007R1

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416

(B) TELEFAX: 415/952-9881

(C) TELEX: 910/371-7168

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: Amino Acid

10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
1 5 10 15
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
20 20 25 30
Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
35 40 45
Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
50 55 60
25 Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
65 70 75
Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
30 80 85 90
Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
95 100 105
35 Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly

110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro
125 130 135

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Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His
140 145 150

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Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys
155 160 165

Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro
170 175 180

15

Thr
181

(2) INFORMATION FOR SEQ ID NO:2:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50

TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTGC AGAGGCTGCC 100

CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150

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ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200

TAATTCTGAA TGTGCCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250
 TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300
 5 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350
 CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400
 ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1438 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50
TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
AGCTCTATCC TGTGCCCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150
TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
CAGAGGGGGC ACCTGGTCGG ACTCGGTGG GCTCGGGCGG CCCC GCCTCC 250
CCCCGCCCCG CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350
AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400
GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450
GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500
AGATTGGTCT GTTTTGTTGC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550
CCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600

AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCCTG 650
 GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700
 5 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750
 CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800
 TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850
 10 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900
 CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950
 15 GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000
 CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050
 GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100
 20 GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTTCA GCCAGCATTC 1150
 CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200
 25 GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250
 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300
 ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350
 30 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400
 TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

35 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
1 5 10 15

Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
20 25 30

Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
15 35 40 45

Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
50 55 60

Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
20 65 70 75

Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
80 85 90

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
95 100 105

Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly
30 110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro
125 130 135

Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His
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|----|---|-----|--|-----|--|-----|
| | | 140 | | 145 | | 150 |
| | Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys | | | | | |
| | | 155 | | 160 | | 165 |
| 5 | Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro | | | | | |
| | | 170 | | 175 | | 180 |
| | Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys | | | | | |
| 10 | | 185 | | 190 | | 195 |
| | Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu | | | | | |
| | | 200 | | 205 | | 210 |
| 15 | Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg | | | | | |
| | | 215 | | 220 | | 225 |
| | His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly | | | | | |
| | | 230 | | 235 | | 240 |
| 20 | Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu | | | | | |
| | | 245 | | 250 | | 255 |
| | Asp Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys | | | | | |
| 25 | | 260 | | 265 | | 270 |
| | Ile Cys Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr | | | | | |
| | | 275 | | 280 | | 285 |
| 30 | Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp | | | | | |
| | | 290 | | 295 | | 300 |
| | Asp Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr | | | | | |
| | | 305 | | 310 | | 315 |
| 35 | | | | | | |

Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met Met Leu Gln
 320 325 330

Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro Ala Arg
 335 340 345

Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu
 350 355 360

Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln
 365 370 375

Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu
 380 385 390

Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
 395 400 405

Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
 410 415 417

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAAGCC 27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10 TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1634 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50

25 ACGGAGCCCG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94
Met Glu

1

30 CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133
Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu

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CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr

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|----|---|
| | CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211 |
| | Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys |
| | 30 35 40 |
| 5 | AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250 |
| | Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly |
| | 45 50 |
| 10 | CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289 |
| | His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn |
| | 55 60 65 |
| 15 | TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328 |
| | Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala |
| | 70 75 80 |
| 20 | TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367 |
| | Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln |
| | 85 90 |
| 25 | GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406 |
| | Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn |
| | 95 100 105 |
| 30 | TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445 |
| | Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro |
| | 110 115 |
| 35 | GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA TGT GTC AGC 484 |
| | Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser |
| | 120 125 130 |
| 35 | AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 523 |
| | Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly |
| | 135 140 145 |

| | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | GCC | CTG | CAC | CGC | CAC | ACA | CGG | CTA | CTC | TGT | TCC | CGC | AGA | 562 |
| | Ala | Leu | His | Arg | His | Thr | Arg | Leu | Leu | Cys | Ser | Arg | Arg | |
| | | | | | 150 | | | | | 155 | | | | |
| 5 | GAT | ACT | GAC | TGT | GGG | ACC | TGC | CTG | CCT | GGC | TTC | TAT | GAA | 601 |
| | Asp | Thr | Asp | Cys | Gly | Thr | Cys | Leu | Pro | Gly | Phe | Tyr | Glu | |
| | | 160 | | | | | 165 | | | | | 170 | | |
| | CAT | GGC | GAT | GGC | TGC | GTG | TCC | TGC | CCC | ACG | AGC | ACC | CTG | 640 |
| 10 | His | Gly | Asp | Gly | Cys | Val | Ser | Cys | Pro | Thr | Ser | Thr | Leu | |
| | | | | 175 | | | | | 180 | | | | | |
| | GGG | AGC | TGT | CCA | GAG | CGC | TGT | GCC | GCT | GTC | TGT | GGC | TGG | 679 |
| | Gly | Ser | Cys | Pro | Glu | Arg | Cys | Ala | Ala | Val | Cys | Gly | Trp | |
| 15 | | 185 | | | | 190 | | | | | 195 | | | |
| | AGG | CAG | ATG | TTC | TGG | GTC | CAG | GTG | CTC | CTG | GCT | GGC | CTT | 718 |
| | Arg | Gln | Met | Phe | Trp | Val | Gln | Val | Leu | Leu | Ala | Gly | Leu | |
| | | | 200 | | | | | 205 | | | | | 210 | |
| 20 | GTG | GTC | CCC | CTC | CTG | CTT | GGG | GCC | ACC | CTG | ACC | TAC | ACA | 757 |
| | Val | Val | Pro | Leu | Leu | Leu | Gly | Ala | Thr | Leu | Thr | Tyr | Thr | |
| | | | | | 215 | | | | | 220 | | | | |
| 25 | TAC | CGC | CAC | TGC | TGG | CCT | CAC | AAG | CCC | CTG | GTT | ACT | GCA | 796 |
| | Tyr | Arg | His | Cys | Trp | Pro | His | Lys | Pro | Leu | Val | Thr | Ala | |
| | | | 225 | | | | | 230 | | | | 235 | | |
| | GAT | GAA | GCT | GGG | ATG | GAG | GCT | CTG | ACC | CCA | CCA | CCG | GCC | 835 |
| 30 | Asp | Glu | Ala | Gly | Met | Glu | Ala | Leu | Thr | Pro | Pro | Pro | Ala | |
| | | | | 240 | | | | | 245 | | | | | |
| | ACC | CAT | CTG | TCA | CCC | TTG | GAC | AGC | GCC | CAC | ACC | CTT | CTA | 874 |
| | Thr | His | Leu | Ser | Pro | Leu | Asp | Ser | Ala | His | Thr | Leu | Leu | |
| 35 | | 250 | | | | | 255 | | | | | 260 | | |

| | | |
|----|---|------|
| | GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG | 913 |
| | Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln | |
| | 265 270 275 | |
| 5 | TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC | 952 |
| | Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr | |
| | 280 285 | |
| 10 | CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC | 991 |
| | Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp | |
| | 290 295 300 | |
| 15 | CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC | 1030 |
| | Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro | |
| | 305 310 | |
| 20 | ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG | 1069 |
| | Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met | |
| | 315 320 325 | |
| 25 | ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC | 1108 |
| | Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp | |
| | 330 335 340 | |
| 30 | GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG | 1147 |
| | Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr | |
| | 345 350 | |
| 35 | CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG | 1186 |
| | Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val | |
| | 355 360 365 | |
| 35 | GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC | 1225 |
| | Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu | |
| | 370 375 | |

AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264
Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala
380 385 390

5 GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303
Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
395 400 405

10 GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
410 415 417

GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAGC 1390

15 CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC 1490

20 CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540

GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGTA 1590

TTAAATCTGT GAAAGAAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1634

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

15
A
G
G
A
T
G
G
G
A
A
G
T
G
T
G
T
G
A
T
A
T
A
T
C
C
T
T
G
A
T